

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 14, 2003, 11:42:22 : Search time 56.379 Seconds

(without alignments)
11410 644 Million cell updates/sec

Title: us-09-910-428-1

Perfect score: 26

Sequence: 1 ggtctaatctttctgtaccag 26

Scoring table: IDENTITY_NUC

Gapop 10 0 Gapext 1 0

Searched: 2054640 seqs 1455102878 residues

Total number of hits satisfying chosen parameters: 4109200

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 98

Maximum Match 100%

Listing first 45 summaries

Database :
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pl:*
10: gb_ro:*
11: gb_sl:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_ov:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sl:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_hum:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pla:*
35: em_htg_rud:*
36: em_htg_mam:*
37: em_htg_vit:*
38: em_sy:*
39: em_htg_hum:*
40: em_htg_mus:*
41: em_htg_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	26	100.0	349	AF126288	AF126288 Bos tauru
2	26	100.0	732	AF040955	AF040955 Bos indic
3	26	100.0	25688	BT015741	BT015741 Bos tauru
4	19.8	76.2	126837	AL451106	AL451106 Human DNA
5	19.6	75.4	144427	AC094612	AC094612 Rattus no
6	19.6	75.4	133621	AC126814	AC126814 Rattus no
7	19.6	75.4	138624	AC101881	AC101881 Mus muscu
8	19.4	74.6	51881	AL158049	AL158049 Human DNA
9	19.2	73.8	115297	U812207	U812207 Homo sapien
10	19.2	73.8	153909	AC124782	AC124782 Rattus no
11	19.2	73.8	156342	AC125295	AC125295 Rattus no
12	19.2	73.8	160091	AC092422	AC092422 Human Chr
13	19.2	72.8	147776	AL592546	AL592546 Human DNA
14	19.2	73.8	187357	AC129388	AC129388 Rattus no
15	19.2	73.8	193446	AC094597	AC094597 Rattus no
16	18.8	72.3	80738	AC119858	AC119858 Mus muscu
17	18.8	72.3	121448	AC092699	AC092699 Homo sapi
18	18.8	72.3	155123	AC129447	AC129447 Rattus no
19	18.8	72.3	163236	AC095804	AC095804 Rattus no
20	18.8	72.3	168374	AL102203	AL102203 Mus muscu
21	18.8	72.3	188374	AC095050	AC095050 Homo sapi
22	18.8	72.3	190070	AC127907	AC127907 Rattus no
23	18.8	72.3	196305	AC090247	AC090247 Homo sapi
24	18.8	72.3	190415	AC066612	AC066612 Homo sapi
25	18.8	72.3	194349	AC094679	AC094679 Homo sapi
26	18.8	72.3	193761	AC092273	AC092273 Homo sapi
27	18.8	72.3	207534	AC092498	AC092498 Homo sapi
28	18.6	71.5	588	BT015741	BT015741 Bos tauru
29	18.6	71.5	588	BT015741	BT015741 Bos tauru
30	18.6	71.5	4669	AD010152	AD010152 Mus muscu
31	18.6	71.5	4669	AD010152	AD010152 Mus muscu
32	18.6	71.5	97037	AC004973	AC004973 Homo sapi
33	18.6	71.5	100166	AC103466	AC103466 Rattus no
34	18.6	71.5	102242	AP004041	AP004041 Oryza sat
35	18.6	71.5	115846	AC104276	AC104276 Oryza sat
36	18.6	71.5	128468	AL139090	AL139090 Human DNA
37	18.6	71.5	144179	AC119524	AC119524 Rattus no
38	18.6	71.5	147765	AC084069	AC084069 Mus muscu
39	18.6	71.5	149094	AC116874	AC116874 Mus muscu
40	18.6	71.5	160354	AC101646	AC101646 Mus muscu
41	18.6	71.5	157274	AP004679	AP004679 Oryza sat
42	18.6	71.5	158966	AC011524	AC011524 Homo sapi
43	18.6	71.5	161520	AC110989	AC110989 Homo sapi
44	18.6	71.5	163498	AC127878	AC127878 Rattus no
45	18.6	71.5	166087	AC092295	AC092295 Homo sapi

ALIGNMENTS

RESULT 1
AF126288 349 bp DNA linear MAY 27 1999
LOCUS AF126288
DEFINITION Bos taurus growth hormone receptor (GHR) gene, promoter and 5' untranslated region.
ACCESSION AF126288
VERSION AF126288.1 GI:4894683
KEYWORDS
SOURCE
ORGANISM
Bos taurus
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE
1 (bases 1 to 349)
Ge,M., Davis,M.F., Hines,H.C. and Ivins,R.M.

Prod. No. is the number of results predicted by chance to have a

COMMENT On Dec 20, 2001 this sequence version replaced g1:15624447.

Center: Baylor College of Medicine
Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc.help@bcm.tmc.edu

Center project name: CH230-541

Center clone name: CH230-541

Assembly program: Phrap version 0.920320First call to findPhrapList

Consensus quality: 133897 bases at least Q40
Consensus quality: 142583 bases at least Q36

Consensus quality: 148654 bases at least Q20

Estimated insert size: 135494; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; average-IP estimation
Quality coverage: 2.1x in Q20 bases; sum-of-contigs estimation

NOTE: Estimated insert size may differ from sequence length
(see <http://www.blast.bcm.tmc.edu/bdb/Genbank/Data/data.html>)

NOTE: This is a 'working draft' sequence. It currently consists of 59 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 9929: contig of 9929 bp in length
9930 10029: gap of unknown length
10030 19562: contig of 9533 bp in length
19563 19662: gap of unknown length
19663 25954: contig of 6292 bp in length
25955 26054: gap of unknown length
26055 31954: contig of 5900 bp in length
31955 32054: gap of unknown length
32055 38036: contig of 6382 bp in length
38036 38537: gap of unknown length
38537 42643: contig of 4107 bp in length
42643 42744: gap of unknown length
42744 47681: contig of 4938 bp in length
47681 47782: gap of unknown length
47782 51504: contig of 3723 bp in length
51505 51604: gap of unknown length
51605 54660: contig of 3056 bp in length
54661 54760: gap of unknown length
54761 59890: contig of 5130 bp in length
59891 59990: gap of unknown length
59991 63789: contig of 3699 bp in length
63790 66997: contig of 3208 bp in length
66998 67097: gap of unknown length
67098 70030: contig of 2933 bp in length
70031 74162: gap of unknown length
74163 74262: gap of unknown length
74263 77599: contig of 3337 bp in length
77600 77699: gap of unknown length
77700 79923: contig of 2224 bp in length
79924 80023: gap of unknown length
80024 82519: contig of 2596 bp in length
82520 82649: gap of unknown length
82650 85120: contig of 2371 bp in length
85121 88663: contig of 3543 bp in length
88664 88763: gap of unknown length
88764 91497: contig of 2734 bp in length
91498 91597: gap of unknown length
91598 93139: contig of 1542 bp in length
93140 93239: gap of unknown length
93240 95302: contig of 2063 bp in length
95303 95402: gap of unknown length

95403 98038: contig of 4636 bp in length
98039 98138: gap of unknown length
98139 102199: contig of 4061 bp in length
102200 102299: gap of unknown length
102300 105343: contig of 3044 bp in length
105344 105443: gap of unknown length
105444 108005: contig of 2562 bp in length
108006 108105: gap of unknown length
108106 109420: contig of 1715 bp in length
109421 109920: gap of unknown length
109921 109921: contig of 2094 bp in length
110115 112015: gap of unknown length
112016 114297: contig of 2183 bp in length
114298 114397: gap of unknown length
114398 116200: contig of 1803 bp in length
116201 116300: gap of unknown length
116301 118540: contig of 2240 bp in length
118541 118640: gap of unknown length
118641 120017: contig of 1377 bp in length
120018 120117: gap of unknown length
120118 121654: contig of 1537 bp in length
121655 121754: gap of unknown length
121755 123040: contig of 1286 bp in length
123041 123140: gap of unknown length
123141 125246: contig of 2106 bp in length
125247 125345: gap of unknown length
125346 127937: contig of 2591 bp in length
127938 128037: gap of unknown length
128038 128965: contig of 1928 bp in length
128966 129665: gap of unknown length
129666 131785: contig of 1720 bp in length
131786 131885: gap of unknown length
131886 134325: contig of 2440 bp in length
134326 134425: gap of unknown length
134426 135449: contig of 1924 bp in length
135450 136449: gap of unknown length
136450 138224: contig of 1775 bp in length
138225 138324: gap of unknown length
138325 139399: contig of 1675 bp in length
139399 140099: gap of unknown length
140100 141317: contig of 1218 bp in length
141318 141417: gap of unknown length
141418 142711: contig of 1294 bp in length
142712 142811: gap of unknown length
142812 145018: contig of 2207 bp in length
145019 145118: gap of unknown length
145119 146940: contig of 1822 bp in length
146941 147040: gap of unknown length
147041 148586: contig of 1546 bp in length
148587 148686: gap of unknown length
148687 149923: contig of 1237 bp in length
149924 150023: gap of unknown length
150024 151413: contig of 1390 bp in length
151414 151513: gap of unknown length
151514 152734: contig of 1221 bp in length
152735 152834: gap of unknown length
152835 153912: contig of 1078 bp in length
153913 154012: gap of unknown length
154013 156181: contig of 2169 bp in length
156182 156281: gap of unknown length
156282 157348: contig of 1067 bp in length
157349 157448: gap of unknown length
157449 158469: contig of 1021 bp in length
158470 158669: gap of unknown length
158670 159681: contig of 1112 bp in length
159682 159781: gap of unknown length
159782 160789: contig of 1008 bp in length
160790 160899: gap of unknown length

Query Match 75.48: Score 19.61 DB 2: Length 164427;
Best Local Similarity 84.68: Pred. No. 1.7e+02;
Matches 22: Conservative 0: Mismatches 4: Indels 0: Gaps 0:

49197	49246	gap of unknown length
49297	51707	contig of 2411 bp in length
51708	51807	gap of unknown length
51808	54110	contig of 2303 bp in length
54111	54210	gap of unknown length
54211	57375	contig of 3165 bp in length
57376	57475	gap of unknown length
57476	60536	contig of 3061 bp in length
60537	60536	gap of unknown length
60537	63317	contig of 2681 bp in length
63318	63417	gap of unknown length
63418	65968	contig of 2551 bp in length
65969	66068	gap of unknown length
66069	69498	contig of 3430 bp in length
69499	69598	gap of unknown length
71527	71526	contig of 1928 bp in length
71527	71626	gap of unknown length
71627	74676	contig of 3050 bp in length
74677	74776	gap of unknown length
74777	77583	contig of 2807 bp in length
77584	77683	gap of unknown length
77684	80148	contig of 2465 bp in length
80149	80248	gap of unknown length
80249	82557	contig of 2393 bp in length
82558	82557	gap of unknown length
82558	84481	contig of 1824 bp in length
84482	84581	gap of unknown length
84582	87302	contig of 2721 bp in length
87303	87402	gap of unknown length
87403	90697	contig of 3295 bp in length
90698	90797	gap of unknown length
90798	93986	contig of 3189 bp in length
93987	94086	gap of unknown length
94087	97550	contig of 3464 bp in length
97551	97650	gap of unknown length
97651	102172	contig of 4522 bp in length
102173	102272	gap of unknown length
102273	105168	contig of 2896 bp in length
105169	105268	gap of unknown length
105269	109192	contig of 3924 bp in length
109193	109292	gap of unknown length
109293	114339	contig of 5047 bp in length
114340	114439	gap of unknown length
114440	118107	contig of 3668 bp in length
118108	118207	gap of unknown length
118208	122652	contig of 4445 bp in length
122653	122752	gap of unknown length
122753	128324	contig of 5572 bp in length
128325	128424	gap of unknown length
128425	133512	contig of 5088 bp in length
133513	133612	gap of unknown length
133613	141318	contig of 7706 bp in length
141319	141418	gap of unknown length
141419	147572	contig of 6154 bp in length
147573	147672	gap of unknown length
147673	156647	contig of 7975 bp in length
156648	155747	gap of unknown length
155748	163030	contig of 7283 bp in length
163031	163130	gap of unknown length
163131	173435	contig of 10305 bp in length
173436	173535	gap of unknown length

Query Match 75.44: Score 19.6; PR 2; Length 183621;
 Best Local Similarity 84.68; Mismatches 4; Indels 0; Gaps 0;
 Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

DB 80065 STGCTTATCTTCTGATCAG 80040
 1 GTCCTATCTTCTGATCAG 26
 ||||| ||||| ||||| |||||

RESULT 7
 AC101881/c

AC101881 198624 bp DNA linear map 21-Aug-2002
 Mus musculus clone H23-387F19, WORKING DRAFT SEQUENCE, 8 unordered
 pieces.
 AC101881.2 GI:22381426
 HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
 SOURCE
 house mouse.
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 198624)
 Birren, B., Nusbaum, C. and Lander, E.
 Mus musculus, clone RP23-387F19
 Unpublished
 2 (bases 1 to 198624)

Birren, B., Lincol, L., Nusbaum, C., Lander, E., All, A., Allen, N.,
 Anderson, S., Barina, N., Bastien, V., Boguslavsky, L., Boukhalter, B.,
 Brown, A., Camarata, J., Campoliano, A., Chang, J., Chararo, B.,
 Choquet, Y., Colangelo, M., Collins, S., Collumore, A., Cook, A.,
 Covey, P., D'Arillano, K., Dewa, K., Diaz, J., Dodge, S., Fero, S.,
 Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardina, S.,
 Ginde, S., Gord, S., Goyette, M., Graham, L., Grand Pierre, N.,
 Hagos, B., Heald, A., Horton, L., Hulme, W., Iliev, I., Johnson, R.,
 Jones, C., Kamat, A., Karatas, A., Kelis, C., Labèque, K.,
 Lamazares, E., Landers, T., Lebecky, J., Levine, R., Liu, G.,
 Maclean, C., Macdonald, P., Major, J., Margus, N., Matthews, C.,
 McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrum, J.,
 Menes, L., Mihova, T., Mienga, V., Murphy, T., Naylor, J., Naylor, C.,
 Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D.,
 Oliver, J., Peterson, K., Phunkhang, P., Pivert, N., Pollara, V.,
 Raymond, C., Rector, R., Rieback, M., Riley, R., Risc, C., Rogov, P.,
 Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupbach, R.,
 Seaman, S., Severy, P., Spencer, B., Stange-Thumann, N., Stojanovic, N.,
 Strauss, N., Subramanian, A., Talamas, J., Testa, S., Theodore, J.,
 Topham, K., Travers, M., Travis, N., Trillito, J., Vassiliev, H.,
 Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W., Young, G.,
 Zehnke, L., Ziemer, A. and Zody, M.

TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 Submitted (43-MAY-2003) Whitehead Institute/MIT Center for Genome
 Research, 330 Charles Street, Cambridge, MA 02141, USA
 3 (bases 1 to 198624)

Birren, B., Nusbaum, C., Lander, E., All, A., Allen, N., Anderson, S.,
 Barina, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhalter, B.,
 Camarata, J., Chang, J., Chararo, B., Choquet, Y., Collumore, A.,
 Cook, A., Covey, P., D'Arillano, K., Dewa, K., Diaz, J., Dodge, S.,
 Fero, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J.,
 Gardina, S., Ginde, S., Graham, L., Grand Pierre, N., Hagos, B.,
 Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A.,
 Karatas, A., Kelis, C., Landers, T., Levine, R., Liu, G.,
 Liu, G., Maclean, C., Macdonald, P., Major, J., Matthews, C.,
 McCarthy, M., Meldrum, J., Menes, L., Mihova, T., Mienga, V.,
 Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H.,
 O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K.,
 Phunkhang, P., Pivert, N., Raymond, C., Rector, R., Risc, C., Rogov, P.,
 Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupbach, R.,
 Seaman, S., Severy, P., Spencer, B., Stange-Thumann, N., Stojanovic, N.,
 Strauss, N., Subramanian, A., Talamas, J., Testa, S., Theodore, J.,
 Topham, K., Travers, M., Travis, N., Trillito, J., Vassiliev, H.,
 Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G.,
 Zehnke, L., Ziemer, A. and Zody, M.

TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 Submitted (43-MAY-2003) Whitehead Institute/MIT Center for Genome
 Research, 330 Charles Street, Cambridge, MA 02141, USA
 On Aug 21, 2002 this sequence version replaced g1:1706067.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.gcc.washington.edu/pub/RepeatMasker.html

Center: Whitehead Institute/MIT Center for Genome Research
 Center code: W1B8
 Web site: http://www.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu
 Project information
 Center project name: L17690

Contig clone name: 187_F_19

Summary Statistics

Sequencing vector: Plasmid; 0/2: 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960781
 Consensus quality: 195624 bases at least Q40
 Consensus quality: 197149 bases at least Q30
 Consensus quality: 197644 bases at least Q20
 Insert size: 194000; agarose-1p
 Insert size: 197924; sum-of-contigs
 Quality coverage: 9.2 in Q20 bases; agarose 1p
 Quality coverage: 9.0 in Q20 bases; sum-of-contigs

- * NOTE: This is a 'working draft' sequence. It currently
- * consists of 8 contigs. The true order of the pieces
- * is not known and their order in this sequence record is
- * arbitrary. Gaps between the contigs are represented as
- * runs of Ns, but the exact sizes of the gaps are unknown.
- * This record will be updated with the finished sequence
- * as soon as it is available and the accession number will
- * be preserved.

1 95762: contig of 95762 bp in length
 * 95763 95862: gap of 100 bp
 * 95863 96510: contig of 648 bp in length
 * 96511 96610: gap of 100 bp
 * 96611 97372: contig of 762 bp in length
 * 97373 97472: gap of 100 bp
 * 97473 98542: contig of 1060 bp in length
 * 98543 98642: gap of 100 bp
 * 98643 112419: contig of 13787 bp in length
 * 112420 112519: gap of 100 bp
 * 112520 135476: contig of 22857 bp in length
 * 135477 135476: gap of 100 bp
 * 135477 171548: contig of 36072 bp in length
 * 171549 171648: gap of 100 bp
 * 171649 198624: contig of 26976 bp in length.
 Location/Qualifiers

FEATURES

SOURCE

1. 198624
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone_lib="RP23 487E19"
 /chromosome="11p15.5" 23 Fongio Mouse HAC"

misc_feature

1.. 95762
 /note="assembly_1-fragment"

misc_feature

vector_end:SP6
 vector_start:SP6

misc_feature

95863.. 96510
 /note="assembly_1-fragment"

misc_feature

96611.. 97372
 /note="assembly_1-fragment"

misc_feature

97473.. 98542
 /note="assembly_1-fragment"

misc_feature

98643.. 112419
 /note="assembly_1-fragment"

misc_feature

112520.. 135476
 /note="assembly_1-fragment"

misc_feature

135477.. 171548
 /note="assembly_1-fragment"

misc_feature

171649.. 198624
 /note="assembly_1-fragment"

misc_feature

clone_end:SP6
 vector_start:SP6

BASE COUNT

62240 a 41171 c 39766 g 54743 t 764 others

Query Match

75.48: Score 19.6; DB 2: Length 198624;

Host Local Similarity

84.68: Prod. No. 1.7e+02;

Matches

22: Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Query

1 GTCCTATCTTTCTGATACAGG 26

DB

184334 GTCCTATCTTTCTGATACAGG 183509

RESULT 8

Accession

AL158049

51881 bp

DNA

linear

PR1 10 SEP-2000

Location

Human DNA sequence from clone RP3-482C21 on chromosome 6, complete

Definition

sequence.

Accession

AL158049

51881 bp

DNA

linear

PR1 10 SEP-2000

Version

AL158049.1

51881 bp

DNA

linear

PR1 10 SEP-2000

Keywords

HTG.

Source

human.

Organism

human.

Reference

Kimberley A.

Title

Direct Submission

Comment

Submitted (30 SEP-2000) Sanger Centre, Hinxton, Cambridgeshire, UK

Reference

Kimberley A.

Title

Direct Submission

Comment

Submitted (30 SEP-2000) Sanger Centre, Hinxton, Cambridgeshire, UK

Reference

Kimberley A.

Title

Direct Submission

Comment

Submitted (30 SEP-2000) Sanger Centre, Hinxton, Cambridgeshire, UK

Reference

Kimberley A.

Title

Direct Submission

Comment

Submitted (30 SEP-2000) Sanger Centre, Hinxton, Cambridgeshire, UK

Reference

Kimberley A.

Title

Direct Submission

Comment

Submitted (30 SEP-2000) Sanger Centre, Hinxton, Cambridgeshire, UK

Reference

Kimberley A.

Title

Direct Submission

Comment

Submitted (30 SEP-2000) Sanger Centre, Hinxton, Cambridgeshire, UK

Reference

Kimberley A.

Title

Direct Submission

Comment

Submitted (30 SEP-2000) Sanger Centre, Hinxton, Cambridgeshire, UK

Reference

Kimberley A.

Title

Direct Submission

Comment

Submitted (30 SEP-2000) Sanger Centre, Hinxton, Cambridgeshire, UK

Reference

Kimberley A.

Title

Direct Submission

Comment

Submitted (30 SEP-2000) Sanger Centre, Hinxton, Cambridgeshire, UK

Reference

Kimberley A.

Title

Direct Submission

Comment

Submitted (30 SEP-2000) Sanger Centre, Hinxton, Cambridgeshire, UK

Reference

Kimberley A.

Title

Direct Submission

Comment

Submitted (30 SEP-2000) Sanger Centre, Hinxton, Cambridgeshire, UK

Reference

Kimberley A.

Title

Direct Submission

Comment

Submitted (30 SEP-2000) Sanger Centre, Hinxton, Cambridgeshire, UK

ordered piece.

ACCESSION U82207
 VERSION 1
 HTG: HTGS_PNASP2: HTGS_CANCELLED.
 KEYWORDS
 SOURCE Homo sapiens
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Smith, D.P.
 TITLE Sequencing of Human Chromosome 10
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 115297)
 AUTHORS Du, L. and Smith, D.
 TITLE Direct Submission
 JOURNAL Submitted (13-DEC-1996) Bioinformatics Division, Genome Therapeutics Corporation 100 Beaver Street, Waltham, MA 02154, USA
 On Dec 9, 1998 this sequence version replaced g1:1773045.
 Note: Clone was sequenced in 1996 using Multiplex DNA Sequencing Technology. Data may contain low quality sequence and BAC/Cosmid vector sequences.

COMMENT
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 1 contigs. Gaps between the contigs
 * are represented as runs of N. The order of the pieces
 * is believed to be correct as given, however the sizes
 * of the gaps between them are based on estimates that have
 * provided by the submitter
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved.
 1 115297: contig of 115297 bp in length.
 Location/Qualifiers
 1. 115297
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="10"
 /map="10q25.1"
 /clone="C11947SK-1119P1"
 RASP COUNT 13880 3 22767 2 23595 3 35055 1
 ORIGIN

Query Match 73.88: Score 19.2: DB 2: Length 115297:
 Best Local Similarity 87.54: P-adj 2.6e-07:
 Matches 21: Conservative 0: Mismatch 3: Indels 0: Gaps 0:

QY 1 GTCCTATATTTTCTCTCTACCA 24
 ||| ||||| ||||| |||||
 Db 99505 GTCATTAATTTTCTCTCTACCA 24482

REPOSITORY 10
 AC124782
 LOCUS
 DEFINITION Rattus norvegicus clone CH230-44703. *** SEQUENCING IN PROGRESS ***
 *** 38 unordered pieces. ***
 AC124782 15309 bp DNA linear HTG 31-JUL-2002
 AC124782.2 C1-21465317
 HTG: HTGS_PNASP1
 KEYWORDS Norway rat
 SOURCE Rattus norvegicus
 ORGANISM Rattus norvegicus

REFERENCE
 AUTHORS Mammalia: Eutheria: Chordata: Craniata: Vertebrata: Euteleostomi:
 Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo.
 1 (bases 1 to 15309)
 Smith, D.P.
 TITLE Sequencing of Human Chromosome 10
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 115297)
 AUTHORS Du, L. and Smith, D.
 TITLE Direct Submission
 JOURNAL Submitted (13-DEC-1996) Bioinformatics Division, Genome Therapeutics Corporation 100 Beaver Street, Waltham, MA 02154, USA
 On Dec 9, 1998 this sequence version replaced g1:1773045.
 Note: Clone was sequenced in 1996 using Multiplex DNA Sequencing Technology. Data may contain low quality sequence and BAC/Cosmid vector sequences.

COMMENT
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 1 contigs. Gaps between the contigs
 * are represented as runs of N. The order of the pieces
 * is believed to be correct as given, however the sizes
 * of the gaps between them are based on estimates that have
 * provided by the submitter
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved.
 1 115297: contig of 115297 bp in length.
 Location/Qualifiers
 1. 115297
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="10"
 /map="10q25.1"
 /clone="C11947SK-1119P1"
 RASP COUNT 13880 3 22767 2 23595 3 35055 1
 ORIGIN

Delaney, K.R., Delgado, O., Dunn, A.L., Ding, Y., Dinh, H.H.,
 Douthett, K.J., Draper, H., Dugan Rocha, S., Durkin, K.T.,
 Eathart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
 Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
 Gadioli, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
 Gorrell, J.H., Guevara, M., Gunaratne, P., Hale, S., Hamilton, K.,
 Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.,
 Hernandez, O., Hodgson, A., Hoque, M., Holloway, C., Hollins, B.,
 Homs, P., Howard, S., Hober, J., Hult, S., Hume, J., Jackson, L.R.,
 Jacobson, B., Jia, Y., Johnson, K., Jolyet, S., Joudah, S.,
 Karlsson, B., Kelly, S., Khan, U., Ning, Y., Koryak, J., Kovar, C.,
 Kratovic, J., Kuresh, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.,
 Li, J., Li, Z., Licharge, U., Lien, C., Liu, J., Liu, W., Lounsbury, H.,
 Lozano, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,
 Maheshwari, M., Kapur, P., Martin, R., Matindale, A., Martinez, R.,
 Massey, E., McWhirry, E., McLeod, M.P., Meador, M., Mei, G., Metzger, M.,
 Miner, G., Miner, D., Mitchell, T., Molabai, K., Morgan, M., Morris, S.,
 Moser, M., Neill, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N.,
 Nguyen, N., Nickerson, E., Norken, S., Oquh, M., Okunolu, G.,
 Orantje, N., Oyler, R., Pace, A., Payton, B., Peery, J., Perez, L.,
 Peters, L., Pickens, R., Primus, E., Pull, L., Quiles, M., Reu, Y.,
 Rives, M., Rojas, A., Rojebokan, I., Rolfe, M., Ruiz, S., Savery, G.,
 Scherer, S., Scott, G., Shen, H., Shoshitani, N., Stinson, I.,
 Sodergren, E., Sonalke, T., Sparks, A., Stanley, H., Stone, H.,
 Sutton, A., Swalek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tany, H.,
 Tasey, J., Taylor, C., Taylor, P., Telford, B., Thomas, R., Thomas, S.,
 Usami, K., Vasquez, L., Vera, V., Villalobos, V., Vinson, R., Wang, S.,
 Wang, S., Ward, Moore, S., Warren, R., Washington, C., Washington, S.,
 Williams, G., Williamson, A., Wlozyk, R., Woodson, S., Worley, K.,
 Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,
 Weinstein, G. and Gibbs, R.

Direct Submission
 2 (bases 1 to 153909)
 Worley, K.C.
 Direct Submission
 Submitted (17-JUN-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 153909)
 Worley, K.C.
 Direct Submission
 Submitted (31-JUL-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Jun 13, 2002 this sequence version replaced g1:2145004.

Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu

Project Information
 Center project name: KAVY
 Center clone name: CH230-44703

Summary Statistics
 Sequencing vector: plasmid
 Chemistry: Dye-terminator Big Dye 3.0% of reads
 Assembly program: Phrap, version 0.940329
 Consensus quality: 124699 bases at least Q40
 Consensus quality: 150127 bases at least Q30
 Consensus quality: 135717 bases at least Q20

NOTE: Estimated insert size may differ from sequence length
 (see http://www.hgsc.bcm.tmc.edu/hgsc/genbank/draft_data.html).
 NOTE: This is a 'working draft' sequence. It currently
 * consists of 38 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
 1 1162: contig of 1162 bp in length

1163	1262:	gap of unknown	length
1263	2412:	contig of 1150	bp in length
2413	2512:	gap of unknown	length
2513	5248:	contig of 2536	bp in length
5049	5148:	gap of unknown	length
5149	6814:	contig of 1666	bp in length
6815	6914:	gap of unknown	length
6915	8702:	contig of 1788	bp in length
8703	8802:	gap of unknown	length
8803	10486:	contig of 1584	bp in length
10487	10486:	gap of unknown	length
10487	12875:	contig of 2390	bp in length
12877	12976:	gap of unknown	length
12977	15600:	contig of 2624	bp in length
15601	15700:	gap of unknown	length
17771	17772:	contig of 2072	bp in length
17773	17872:	gap of unknown	length
17873	19852:	contig of 1980	bp in length
19853	19952:	gap of unknown	length
19953	22945:	contig of 2993	bp in length
22945	23045:	gap of unknown	length
23045	25738:	contig of 3753	bp in length
25699	26898:	gap of unknown	length
26899	29328:	contig of 2430	bp in length
29329	29928:	gap of unknown	length
29929	32779:	contig of 3351	bp in length
32780	32879:	gap of unknown	length
32880	35857:	contig of 2178	bp in length
35058	35157:	gap of unknown	length
35158	37461:	contig of 2324	bp in length
37482	37561:	gap of unknown	length
37582	39870:	contig of 2289	bp in length
39871	39970:	gap of unknown	length
39971	42185:	contig of 2215	bp in length
42186	42285:	gap of unknown	length
42286	44726:	contig of 2441	bp in length
44727	44825:	gap of unknown	length
44827	47847:	contig of 3011	bp in length
47838	47937:	gap of unknown	length
47938	51252:	contig of 3275	bp in length
51213	51312:	gap of unknown	length
51313	57113:	contig of 5819	bp in length
57212	57211:	gap of unknown	length
57232	61394:	contig of 4163	bp in length
61395	61494:	gap of unknown	length
61495	65007:	contig of 3513	bp in length
65008	65107:	gap of unknown	length
65108	69017:	contig of 3910	bp in length
69018	69117:	gap of unknown	length
69118	73160:	contig of 4043	bp in length
73161	73260:	gap of unknown	length
73261	79853:	contig of 6534	bp in length
79804	79903:	gap of unknown	length
79904	84613:	contig of 4710	bp in length
84614	84713:	gap of unknown	length
84714	90271:	contig of 5558	bp in length
90272	90371:	gap of unknown	length
90372	95397:	contig of 4336	bp in length
95398	95207:	gap of unknown	length
95208	100696:	contig of 5469	bp in length
100697	100796:	gap of unknown	length
100797	108126:	contig of 7310	bp in length
108127	108226:	gap of unknown	length
108227	115091:	contig of 6985	bp in length
115092	115191:	gap of unknown	length
115192	122209:	contig of 7018	bp in length
122210	122309:	gap of unknown	length
122310	128944:	contig of 6625	bp in length
128945	129044:	gap of unknown	length
129045	134082:	contig of 5048	bp in length
134083	134182:	gap of unknown	length
134183	142105:	contig of 7963	bp in length
142106	142205:	gap of unknown	length

[illegible]

JOURNAL
2 (bases 1 to 156942)
REFERENCE
AUTHORS
TITLE
JOURNAL
Submitted (22-07-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 156942)
REFERENCE
AUTHORS
TITLE
JOURNAL
Submitted (11-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

Center: Baylor College of Medicine
Genome Center
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu>
Contact: hgsc-help@bcm.tmc.edu

Project information
Center project name: GDB
Center clone name: CH230-9A11

Summary statistics
Sequencing vector: plasmid;
Chemistry: dye terminator Big Dye 1000 of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 110586 bases at least Q40
Consensus quality: 115829 bases at least Q30
Consensus quality: 119348 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/hgsc/submit_data.html)
* NOTE: This is a 'working draft' sequence. It currently
* consists of 59 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 1007: contig of 1007 bp in length
* 1008 1107: gap of unknown length
* 1109 2347: contig of 1240 bp in length
* 2348 2447: gap of unknown length
* 2449 3631: contig of 1184 bp in length
* 3632 3732: gap of unknown length
* 3733 4971: contig of 1240 bp in length
* 4972 5072: gap of unknown length
* 5073 6292: contig of 1221 bp in length
* 6293 6392: gap of unknown length
* 6393 8135: contig of 1743 bp in length
* 8136 8235: gap of unknown length
* 8236 9680: contig of 1445 bp in length
* 9681 9781: gap of unknown length
* 9782 10866: contig of 1086 bp in length
* 10867 10966: gap of unknown length
* 10967 12755: contig of 1789 bp in length
* 12756 12855: gap of unknown length
* 12856 14226: contig of 1371 bp in length
* 14227 14327: gap of unknown length
* 14328 15527: contig of 1201 bp in length
* 15528 15627: gap of unknown length
* 15628 16668: contig of 1041 bp in length
* 16669 16768: gap of unknown length
* 16769 18505: contig of 1737 bp in length
* 18506 18605: gap of unknown length
* 18606 19771: contig of 1166 bp in length
* 19772 20954: gap of unknown length
* 20955 21954: contig of 1083 bp in length
* 21955 23215: gap of unknown length
* 23216 24700: contig of 2161 bp in length
* 24701 24800: gap of unknown length
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* 24801 25986: contig of 1186 bp in length
* 25987 26987: gap of unknown length
* 26988 27632: contig of 1546 bp in length
* 27633 27732: gap of unknown length
* 27733 29722: contig of 1989 bp in length
* 29723 29822: gap of unknown length
* 29823 31292: contig of 1470 bp in length
* 31293 31392: gap of unknown length
* 31393 33459: contig of 2068 bp in length
* 33460 33559: gap of unknown length
* 33560 34894: contig of 1335 bp in length
* 34895 36115: gap of unknown length
* 36116 36215: contig of 1121 bp in length
* 36216 37667: gap of unknown length
* 37668 38067: contig of 1752 bp in length
* 38068 40967: gap of unknown length
* 40968 42700: contig of 1733 bp in length
* 42701 42800: gap of unknown length
* 42801 45132: contig of 2311 bp in length
* 45133 45232: gap of unknown length
* 45233 48269: contig of 3037 bp in length
* 48270 48369: gap of unknown length
* 48370 50511: contig of 2142 bp in length
* 50512 52607: gap of unknown length
* 52608 52706: contig of 1996 bp in length
* 52707 55721: gap of unknown length
* 55722 55821: contig of 1015 bp in length
* 55822 54909: gap of unknown length
* 54910 58510: contig of 2588 bp in length
* 58511 61633: gap of unknown length
* 61634 61732: contig of 3123 bp in length
* 61733 64083: gap of unknown length
* 64084 64189: contig of 2357 bp in length
* 64190 66634: gap of unknown length
* 66635 66734: contig of 2445 bp in length
* 66735 66819: gap of unknown length
* 66820 69919: contig of 3085 bp in length
* 69920 72224: gap of unknown length
* 72225 72325: contig of 2305 bp in length
* 72326 75641: gap of unknown length
* 75642 77985: contig of 317 bp in length
* 77986 78085: gap of unknown length
* 78086 80903: contig of 2244 bp in length
* 80904 80910: gap of unknown length
* 80911 83100: contig of 2191 bp in length
* 83101 83200: gap of unknown length
* 83201 86457: contig of 3257 bp in length
* 86458 86557: gap of unknown length
* 86558 87618: contig of 1061 bp in length
* 87619 92388: gap of unknown length
* 92389 92488: contig of 2670 bp in length
* 92489 94059: gap of unknown length
* 94060 94159: contig of 1571 bp in length
* 94160 97505: gap of unknown length
* 97506 97601: contig of 3441 bp in length
* 97602 100407: gap of unknown length
* 100408 100507: contig of 2807 bp in length
* 100508 103939: gap of unknown length
* 103940 104039: contig of 3432 bp in length
* 104040 106122: gap of unknown length
* 106123 108412: contig of 4273 bp in length
* 108413 112122: gap of unknown length
* 112123 112221: contig of 3709 bp in length
* 112222 115704: gap of unknown length
* 115705 115804: contig of 3483 bp in length
* 115805 122058: gap of unknown length
* 122059 122158: contig of 6254 bp in length
* 122159 126727: gap of unknown length
* 126728 126727: contig of 4569 bp in length

* 126728 126927: gap of unknown length

Query Match 73.8% Score 19.22 DB 9: Length 156012;
Best Local Similarity 87.5% Prod No. 2.6e+02;
Matches 21: Conservative 0: Mismatches 4: Indels 0: Gaps 0:

1 GAGTAAATCTTCTCTGACCA 26
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Db 100928 GGTCTAAATCTTCTCTGACCA 100951

RESULT 12
AC002422 160091 bp DNA linear PRI 30-JAN-1998
LOCUS Human Chromosome X, complete sequence.
DEFINITION AC002422
ACCESSION AC002422.1 GI:2826450
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
DIRECT SUBMISSION
2 (bases 1 to 160091)
Bromstein,H.H., States,D.J. and Mazarrella,R.
Submitted (12-AUG-1997) Center for Genetics in Medicine, Box 8232,
Washington University School of Medicine, 4566 Scott Avenue, St.
Louis, MO 63110, USA
4 (bases 1 to 160091)
Bromstein,H.H., States,D.J. and Mazarrella,R.
Submitted (10-JAN-1998) Center for Genetics in Medicine, Box 8232,
Washington University School of Medicine, 4566 Scott Avenue, St.
Louis, MO 63110, USA

REFERENCE
AUTHORS
TITLE
JOURNAL
DIRECT SUBMISSION
2 (bases 1 to 160091)
Bromstein,H.H., States,D.J. and Mazarrella,R.
Submitted (10-JAN-1998) Center for Genetics in Medicine, Box 8232,
Washington University School of Medicine, 4566 Scott Avenue, St.
Louis, MO 63110, USA

COMMENT
Current status of this project is available at:
<http://www.fhc.fhc.edu/seq/seq1/fhcproj1.htm>
Submitted by:
Elison Chen,
Advanced Center for Genetic Technology,
Applied Biosystems Division of Perkin Elmer Corp.,
850 Lincoln Center Drive,
Foster City, CA 94404 USA
e-mail: elison.chen@appliedbiosystems.com

and
Buddy Brownstein,
Center for Genetics in Medicine,
Washington University School of Medicine, Box 8232,
4566 Scott Avenue,
St. Louis, MO 63110, USA
e-mail: buddy@genetics.wustl.edu

FEATURES
source
David J. States,
Institute for Biomedical Computing
Washington University in St. Louis
700 South Euclid Ave.,
St. Louis, MO 63108 USA
e-mail: states@bioc.wustl.edu,
local.jon@qualifiers
1. 160091
/organism="Homo sapiens"
/db="xref="taxon:9606"
/clone_lib="RP11-211N11"

BASE COUNT 49262 a 29505 c 30257 g 51067 t
ORIGIN

Query Match 73.8% Score 19.22 DB 9: Length 160091;
Best Local Similarity 87.5% Prod No. 2.6e+02;
Matches 21: Conservative 0: Mismatches 4: Indels 0: Gaps 0:

1 GAGTAAATCTTCTCTGACCA 24
|||||
Db 88522 GGTCTAAATCTTCTCTGACCA 88545

RESULT 13
AL592546 174776 bp DNA linear PRI 15 NOV 2001
LOCUS Human DNA sequence from clone RP11-211N11 on chromosome 10,
complete sequence.
DEFINITION AL592546
ACCESSION AL592546.7 GI:15591647
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
DIRECT SUBMISSION
Submitted (15 NOV 2001) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humgen@sanger.ac.uk. Clone requests: clone@casal.sanger.ac.uk
On Sep 12, 2001 this sequence version replaced g1:15041956.
During sequence assembly data is completed from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats, all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: EM, EMBL, SW,
SWISSPROT, Tr, TrEMBL, WPI, WORMPEP. Information on the WormPEP
database can be found at
<http://www.sanger.ac.uk/wormpep/>
This sequence is from the library RP11-211N11 constructed by the group
of Peter de Jong. For further details see
<http://www.fhc.fhc.edu/seq/seq1/fhcproj1.htm>
VECTOR: pBlue3.6
This sequence is the entire insert of clone RP11-211N11.
Location/Qualifiers
1. 174776

FEATURES
source
/organism="Homo sapiens"
/db="xref="taxon:9606"
/chromosome="10"
/clone="RP11-211N11"
/clone_lib="RP11-211N11"

BASE COUNT 51535 a 35292 c 35407 g 52542 t
ORIGIN
Query Match 73.8% Score 19.22 DB 9: Length 174776;
Best Local Similarity 87.5% Prod No. 2.6e+02;
Matches 21: Conservative 0: Mismatches 4: Indels 0: Gaps 0:

1 GGTCTAAATCTTCTCTGACCA 24
|||||
Db 109754 GGTCTAAATCTTCTCTGACCA 109731

RESULT 14
AC129388
LOCUS
DEFINITION
AC129388 18757 bp. DNA linear H19.29.202.2002
Rattus norvegicus clone CH230 JCB, *** SEQUENCING IN PROGRESS ***
65 unordered pieces.
AC129388
AC129388.1.01.22001469
http://ncbi.nlm.nih.gov/GenBank/AC129388.1
Rattus norvegicus
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
AUTHORS
1 (bases 1 to 187357)
Muzny, D.M., Adams, C., Adio-Oduola, B., All-ouman, F.R., Allen, C.,
Alsbrooks, S.J., Amaral, H.C., Are, J.R., Ayala, M., Banks, T.,
Barbieri, J., Beutler, J., Bimonte, K., Blackburn, K., Bonin, U.,
Bouck, J., Bowe, S., Brilwa, M., Brown, M., Brown, N.,
Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
Carroll, T.F., Carter, M., Cavazos, S.F., Chacko, J., Chaves, F.,
Chen, G., Chen, R., Chen, Z., Choudhry, J., Christopoulos, C.,
Cleveland, C.B., Cui, C., Dey, M.E., Dethlefsen, S.F., David, R.,
David, M.L., Davis, C., Davy-Carroll, J., Dederich, A.,
DeLaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
Donthwajit, K.T., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
Earhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
Fallis, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Fratitz, P.,
Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, P.,
Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.,
Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.,
Hernandez, O., Hudson, A., Hughes, M., Hultway, C., Hultin, R.,
Husni, F., Howard, S., Huber, T., Hulse, S., Hume, T., Jackson, L.E.,
Jacobson, R., Jia, Y., Johnson, R., Jolyet, S., Joudah, S.,
Karlsson, B., Kelly, S., Khan, U., King, L., Korvan, J., Kovar, C.,
Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.,
Li, J., Li, Z., Lickhage, O., Liu, C., Liu, J., Liu, W., Loubeged, H.,
Lozano, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,
Maheshwari, M., Mapua, F., Martin, R., Martindale, A., Martinez, E.,
Massey, E., Mawhney, E., McLeod, M.P., Meador, M., Mel, G., Metzger, M.,
Miner, C., Miner, T., Mitchell, T., Mohabut, K., Morgan, M., Morris, S.,
Mosier, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N.,
Nguyen, N., Nickerson, E., Nwokwu, S., Ogih, M., Okuyama, G.,
Oguzkaya, N., Ouellet, P., Page, A., Payton, B., Percy, T., Peretz, I.,
Peters, L., Pickett, F., Primus, E., Pui, L., Quille, M., Ren, Y.,
Rives, M., Rojas, A., Polubokan, I., Rolfe, M., Ruiz, S., Savary, G.,
Schuch, S., St. G., St. G., St. G., St. G., St. G., St. G., St. G.,
Sodergren, P., Sonajko, T., Sparks, A., Stanley, H., Strong, M.,
Sutton, A., Swack, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H.,
Tansey, J., Taylor, C., Taylor, T., Telford, R., Thomas, N., Thomas, S.,
Usmani, K., Vasquez, L., Vera, V., Villalón, P., Vinson, P., Wang, Q.,
Wang, S., Ward-Moore, S., Warren, R., Washington, C., Wallington, S.,
Williams, C., Williamson, A., Wleczky, P., Wroden, S., Worley, K.,
Wu, C., Wu, Y., Wu, Y., Zhou, J., Zaitilla, S., Nelson, D.,
Weinstock, G., and Gibbs, R.
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Submitted (29-Jul-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
Project Information
Center project name: gkky
Center clone name: CH230-9C8
Summary Statistics

Sequencing vector: Plasmid:
Chemistry: Dye terminator Big Dye, 100% of reads
Assembly program: Phrap; version 0.940329
Consensus quality: 139705 bases at least Q40
Consensus quality: 146155 bases at least Q30
Consensus quality: 153614 bases at least Q20
NOTE: Estimated insert size may differ from sequence length
(see http://www.lasb.bcm.tmc.edu/dm/genbank_draai_data.html).
NOTE: This is a 'working draft' sequence. It currently
consists of 65 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.

1	1046:	contig of 1046 bp in length
1047	1146:	gap of unknown length
1147	1240:	contig of 1094 bp in length
1241	1340:	gap of unknown length
1341	1440:	contig of 1224 bp in length
1441	1540:	gap of unknown length
1541	1640:	contig of 1156 bp in length
1641	1740:	gap of unknown length
1741	1840:	contig of 1045 bp in length
1841	1940:	gap of unknown length
1941	2040:	contig of 1033 bp in length
2041	2140:	gap of unknown length
2141	2240:	contig of 1192 bp in length
2241	2340:	gap of unknown length
2341	2440:	contig of 2001 bp in length
2441	2540:	gap of unknown length
2541	2640:	contig of 1718 bp in length
2641	2740:	gap of unknown length
2741	2840:	contig of 1347 bp in length
2841	2940:	gap of unknown length
2941	3040:	contig of 2209 bp in length
3041	3140:	gap of unknown length
3141	3240:	contig of 1705 bp in length
3241	3340:	gap of unknown length
3341	3440:	contig of 1862 bp in length
3441	3540:	gap of unknown length
3541	3640:	contig of 1619 bp in length
3641	3740:	gap of unknown length
3741	3840:	contig of 1812 bp in length
3841	3940:	gap of unknown length
3941	4040:	contig of 1668 bp in length
4041	4140:	gap of unknown length
4141	4240:	contig of 1851 bp in length
4241	4340:	gap of unknown length
4341	4440:	contig of 1387 bp in length
4441	4540:	gap of unknown length
4541	4640:	contig of 1261 bp in length
4641	4740:	gap of unknown length
4741	4840:	contig of 1204 bp in length
4841	4940:	gap of unknown length
4941	5040:	contig of 1462 bp in length
5041	5140:	gap of unknown length
5141	5240:	contig of 1752 bp in length
5241	5340:	gap of unknown length
5341	5440:	contig of 1856 bp in length
5441	5540:	gap of unknown length
5541	5640:	contig of 2485 bp in length
5641	5740:	gap of unknown length
5741	5840:	contig of 1330 bp in length
5841	5940:	gap of unknown length
5941	6040:	contig of 1682 bp in length
6041	6140:	gap of unknown length
6141	6240:	contig of 1680 bp in length
6241	6340:	gap of unknown length
6341	6440:	contig of 1574 bp in length
6441	6540:	gap of unknown length

Sequencing vector: Plasmid;
 Chemistry: Dye-terminator Big Dye 100% of reads
 Assembly program: Phrap; version 0.993329
 Consensus quality: 96813 bases at least Q40
 Consensus quality: 103408 bases at least Q30
 Consensus quality: 107911 bases at least Q20

NOTE: Estimated insert size may differ from sequence length
 (see http://www.biotwin.com/seqtech/submit_data.html)
 NOTE: This is a 'working draft' sequence. It currently
 consists of 44 contigs. The true order of the pieces
 is not known and their order in this sequence record is
 arbitrary. Gaps between the contigs are represented as
 runs of N, but the exact sizes of the gaps are unknown.
 This record will be updated with the finished sequence
 as soon as it is available and the accession number will
 be preserved.

1 1664: contig of 1664 bp in length
 * 1665: gap of unknown length
 * 1765: contig of 1351 bp in length
 * 3116: gap of unknown length
 * 3216: contig of 1005 bp in length
 * 4221: gap of unknown length
 * 4321: contig of 1130 bp in length
 * 5451: gap of unknown length
 * 5551: contig of 1271 bp in length
 * 6821: gap of unknown length
 * 6921: contig of 1400 bp in length
 * 8322: gap of unknown length
 * 8422: contig of 1091 bp in length
 * 9511: gap of unknown length
 * 9611: contig of 1186 bp in length
 * 10799: gap of unknown length
 * 10899: contig of 1341 bp in length
 * 12340: gap of unknown length
 * 12340: contig of 1020 bp in length
 * 13460: gap of unknown length
 * 13460: contig of 1401 bp in length
 * 14861: gap of unknown length
 * 14961: contig of 1612 bp in length
 * 16573: gap of unknown length
 * 16573: contig of 1079 bp in length
 * 17552: gap of unknown length
 * 17552: contig of 1305 bp in length
 * 19157: gap of unknown length
 * 19257: contig of 1186 bp in length
 * 20443: gap of unknown length
 * 20443: contig of 1528 bp in length
 * 21771: gap of unknown length
 * 21771: contig of 1106 bp in length
 * 23036: gap of unknown length
 * 23036: contig of 1228 bp in length
 * 24365: gap of unknown length
 * 24365: contig of 1401 bp in length
 * 25866: gap of unknown length
 * 25866: contig of 1002 bp in length
 * 26968: gap of unknown length
 * 27068: contig of 1335 bp in length
 * 28403: gap of unknown length
 * 28503: contig of 1078 bp in length
 * 29581: gap of unknown length
 * 29581: contig of 1188 bp in length
 * 30869: gap of unknown length
 * 30869: contig of 1210 bp in length
 * 32179: gap of unknown length
 * 32279: contig of 1085 bp in length
 * 33364: gap of unknown length
 * 33464: contig of 1462 bp in length
 * 34926: gap of unknown length
 * 35026: contig of 1232 bp in length
 * 36258: gap of unknown length
 * 36358: contig of 1616 bp in length
 * 37974: gap of unknown length
 * 38073: gap of unknown length

38074: contig of 1248 bp in length
 * 39322: gap of unknown length
 * 39422: contig of 1170 bp in length
 * 40591: gap of unknown length
 * 40592: contig of 1438 bp in length
 * 42129: gap of unknown length
 * 42130: contig of 1454 bp in length
 * 42230: gap of unknown length
 * 43684: contig of 1118 bp in length
 * 43754: gap of unknown length
 * 43802: contig of 1726 bp in length
 * 45002: gap of unknown length
 * 45002: contig of 1238 bp in length
 * 46728: gap of unknown length
 * 46828: contig of 1198 bp in length
 * 48066: gap of unknown length
 * 48166: contig of 1931 bp in length
 * 49464: gap of unknown length
 * 49464: contig of 1940 bp in length
 * 51395: gap of unknown length
 * 51495: contig of 1517 bp in length
 * 53435: gap of unknown length
 * 53435: contig of 1993 bp in length
 * 55352: gap of unknown length
 * 55352: contig of 1993 bp in length
 * 56545: gap of unknown length
 * 56545: contig of 1481 bp in length
 * 58126: gap of unknown length
 * 58126: contig of 2008 bp in length
 * 60333: gap of unknown length
 * 60333: contig of 1232 bp in length
 * 62340: gap of unknown length
 * 62340: contig of 1106 bp in length
 * 63643: gap of unknown length
 * 63643: contig of 1696 bp in length
 * 64949: gap of unknown length
 * 64949: contig of 2394 bp in length
 * 66745: gap of unknown length
 * 66745: contig of 2600 bp in length
 * 69239: gap of unknown length
 * 69239: contig of 1544 bp in length
 * 71839: gap of unknown length
 * 71839: contig of 1575 bp in length
 * 73483: gap of unknown length
 * 73483: contig of 2182 bp in length
 * 75158: gap of unknown length
 * 75158: contig of 1878 bp in length
 * 77440: gap of unknown length
 * 77440: contig of 1507 bp in length
 * 79518: gap of unknown length
 * 79518: contig of 1484 bp in length
 * 81025: gap of unknown length
 * 81025: contig of 1484 bp in length
 * 81125: gap of unknown length
 * 81125: contig of 1484 bp in length

Query Match: 73.8% Score 19.2; DB 2; Length 19446;
 Best Local Similarity: 87.5% Pref. No. 2.5e-03;
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Oy 3 GCGTATCTTCTGACACG 26
 UG 74593 GTCATCTTCTGACACG 74570

Search completed: January 14 2003, 14:04:38
 Job time: 383.313 secs

100

100

100

100

100